Specification Amendments

Please replace the Title with the following Title:

METHODS FOR SELECTING NUCLEIC ACID SAMPLE PAIR ~~EVALUATING TISSUE PAIR~~ COMBINATIONS FOR USE IN NUCLEIC ACID ARRAY TECHNOLOGY

Please replace the paragraph at page 11, line 24, to page 12, line 2, with the following paragraph:

The terms "reporter", "label" "detectable reporter" and "detectable label" are used herein to refer to a molecule capable of detection, including, but not limited to, radioactive isotopes, fluorescers, chemiluminescers, enzymes, enzyme substrates, enzyme cofactors, enzyme inhibitors, dyes, metal ions, metal sols, other suitable detectable markers such as biotin or haptens and the like. The term "fluorescer" refers to a substance or portion thereof which is capable of exhibiting fluorescence in the detectable range. The term "cofactor" is used broadly herein to include any molecular moiety that participates in an enzymatic reaction. Particular example of labels which may be used under the invention include, but are not limited to, fluorescein, 5(6)-carboxyfluorescein, Cyanine 3 (CY3 dye~~Cy3~~), Cyanine 5 (CY5 dye~~Cy5~~), rhodamine, dansyl, umbelliferone, TEXAS RED dye~~Texas red~~, luminal, NADPH, horseradish peroxidase and α,β-galactosidase.

Please replace the paragraph at page 45, lines 28-32, with the following paragraph:

All of the experiments were performed and the data obtained using a Mouse Test microarray from Agilent Technologies Inc., Palo Alto, CA. This microarray contains 10 probes of 2150 mouse genes. The genes were obtained from the Incyte ZOOSEQ~~ZooSeq~~ database (Palo Alto, CA) and were selected based on uniqueness of the hits for that gene and the number of clones for that gene present in the ZOOSEQ~~ZooSeq~~ database.

Please replace the paragraph under the ABSTRACT OF THE DISCLOSURE on page 56 with the following paragraph:

Methods are disclosed for selecting a combination of nucleic acid sample pairs for evaluating the ability of an oligonucleotide probe to measure differential expression of genes. Differential gene expression experiments are conducted using (i) nucleic acid sample pairs and (ii) nucleic acid probes immobilized on a substrate, the probes representing a set of genes. The number of genes in the set is a portion of an expected number of genes in a sample. A nucleic acid sample pair combination is selected based on the members of the combination having a maximized number of genes from the set of genes that exhibit differential expression and a minimized number of the genes that do not exhibit differential expression. Methods are also disclosed for identifying a sequence of a nucleic acid that is suitable for use as a substrate surface immobilized probe for a target nucleic acid, for producing an array of nucleic acids on the surface of a substrate and for detecting the presence of nucleic acids on the surface of a substrate.